

CLAIMS

What is claimed is:

- 1 1. A method for separating nucleic acid molecules which have
2 specific alleles, comprising:
 - 3 (a) hybridizing a nucleic acid comprising a heterosequence site
4 with at least one nucleic acid primer specific to the heterosequence site to form a
5 hybridized nucleic acid sequence, wherein the at least one specific nucleic acid
6 primer is capable of undergoing elongation only when hybridized to the
7 heterosequence site;
 - 8 (b) subjecting the hybridized nucleic acid sequence to conditions
9 which permit elongation of the at least one nucleic acid primer; and
 - 10 (c) separating the hybridized nucleic acid sequences which have
11 undergone elongation from the nucleic acid sequences from unhybridized nucleic
12 acid sequences and the nucleic acid primers which have not undergone elongation.
- 1 2. The method of claim 1, wherein the 3' end of the at least one
2 nucleic acid primer corresponds in position to a polymorphic base within the
3 heterosequence site and the nucleic acid primer is capable of undergoing elongation
4 only when the 3' end of the at least one nucleic acid primer is complementary to and
5 hybridized to the polymorphic base within the heterosequence site.
- 1 3. The method of claim 2, wherein one of the primer or one of
2 the elongated primer is labeled with a detection molecule and (d) further comprises
3 separating the hybridized nucleic acid sequences which have undergone elongation
4 utilizing the detection molecule.

1 4. The method of claim 1, further comprising:

2 (d) amplifying the nucleic acid molecule comprising the
3 heterosequence site prior to hybridization with the at least one nucleic acid
4 primer; and

5 (e) identifying the heterosequence site.

1 5. The method of claim 1 wherein the heterosequence site
2 comprises a single nucleotide polymorphism.

1 6. A kit for separating nucleic acid molecules which have
2 specific alleles comprising instructions for carrying out the method of claim 1.

1 7. A method for separating a nucleic acid molecule which has a
2 specific allele, comprising:

3 (a) hybridizing a nucleic acid comprising one or more
4 heterosequence sites with at least one nucleic acid primer specific to the
5 heterosequence site and a ligation primer to form a hybridized nucleic acid
6 sequence, wherein the 3' end of the at least one nucleic acid primer corresponds in
7 position to a polymorphic base within the heterosequence site and the 5' end of the
8 ligation primer is adjacent to the 3' end of the at least one nucleic acid primer;

9 (b) subjecting the at least one nucleic acid primer and the ligation
10 primer to conditions which permit ligation of the at least one nucleic acid primer
11 and the ligation primer; and

12 (c) separating the hybridized nucleic acid molecule in which the
13 primers have undergone ligation.

1 8. The method of claim 7 wherein one of the at least one nucleic
2 acid primer and the ligation primer is labeled with a detection molecule and (c)
3 further comprises separating the hybridized nucleic acid sequences which have
4 undergone elongation utilizing the detection molecule.

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1 9. The method of claim 8 wherein the at least one nucleic acid
2 primer comprises a plurality of primers having different sequences and each
3 sequence is associated with a particular detection molecule such that no two
4 sequences are associated with the same detection molecule.

1 10. A kit for separating a nucleic acid molecule which has a
2 specific allele comprising instructions for carrying out the method of claim 7.

1 11. A method for separating a nucleic acid molecule which has a
2 specific allele, comprising:

3 (a) hybridizing a nucleic acid comprising one or more
4 heterosequence sites with at least one nucleic acid primer specific to the
5 heterosequence site to form hybridized nucleic acid complexes; and

6 (b) separating the hybridized nucleic acid complexes which have
7 complete complementary hybridization from the hybridized nucleic acid complexes
8 which do not have complete complementary hybridization.

1 12. The method of claim 11 further comprising determining the
2 sequence of the nucleic acid comprising the one or more heterosequence sites.

1 13. The method of claim 11 wherein step (b) comprises heating
2 the hybridized nucleic acid complexes to a temperature at which the nucleic acid
3 complexes which do not have complete complementary hybridization dissociate and
4 which the nucleic acid complexes which have complete complementary
5 hybridization do not dissociate.

1 14. The method of claim 11 wherein the at least one nucleic acid
2 primer is labeled with a detection molecule.

1 15. A kit for separating a nucleic acid molecule which has a
2 specific allele comprising instructions for carrying out the method of claim 11.

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1 16. A method for separating a nucleic acid molecule which has a
2 specific allele, comprising:

3 (a) hybridizing a nucleic acid comprising at least a 5'
4 heterosequence site and a 3' heterosequence site with a hetero primer specific to the
5 3' heterosequence site and a homo primer to form a hybridized nucleic acid
6 sequence, wherein the 3' end of the hetero primer corresponds in position to a
7 polymorphic base within the 3' heterosequence site, the homo primer is capable of
8 hybridizing to the nucleic acid at a position located 5' of the 5' heterosequence site
9 and the hetero primer is capable of undergoing elongation only when the 3' end of
10 the hetero primer is complementary to and hybridized to the polymorphic base
11 within the 3' heterosequence site;

12 (b) elongating the hybridized hetero primer such that the nucleic
13 acid sequence between the hetero primer and the homo primer is produced and
14 includes the 5' heterosequence site; and

15 (c) determining the identity of the 5' heterosequence site.

1 17. The method of claim 16 further comprising:

2 (d) utilizing the identity of the 5' heterosequence site to produce
3 another hetero primer and another homo primer, wherein the 3' end of the another
4 hetero primer corresponds in position to a polymorphic base within the 5'
5 heterosequence site, the 5' heterosequence is located 3' to another 5'
6 heterosequence, the homo primer is capable of hybridizing to the nucleic acid at a
7 position located 5' of the another 5' heterosequence site and the hetero primer is
8 capable of undergoing elongation only when the 3' end of the hetero primer is
9 complementary to and hybridized to the polymorphic base within the 5'
10 heterosequence site;

11 (e) hybridizing nucleic acid sequence with the another hetero
12 primer and the another homo primer; and

13 (f) repeating steps (a) through (e) one or more times.

1 21. A method for identifying an allele in a nucleic acid molecule
2 comprising instructions for carrying out the method of claim 20.